

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Bruce William Tedeschi Examiner #: 78150 Date: 2/1/01
 Art Unit: 1642 Phone Number 306-4823 Serial Number: 09/481990
 Mail Box and Bldg/Room Location: CM1/Room Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: FAMILY OF MAMMALIAN POTASSIUM channels, Their cloning

Inventors (please provide full names): FLORIAN LISAGE, ERIC GUILLEMARE, Michael FINK, Fabrice DUPONT, et al.

Earliest Priority Filing Date: Jan 11, 2000

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

SEQ ID# 1

SEQ ID# 2

STAFF USE ONLY

Searcher: B. Smith
 Searcher Phone #: 308-4477
 Searcher Location: CM1-1E7
 Date Searcher Picked Up: 2/2/01
 Date Completed: 2/21/01
 Searcher Prep & Review Time: _____
 Clerical Prep Time: 3
 Online Time: _____

Type of Search

NA Sequence (#) 1
 AA Sequence (#) 1
 Structure (#) _____
 Bibliographic _____
 Litigation _____
 Fulltext _____
 Patent Family _____
 Other _____

Vendors and cost where applicable

STN _____
 Dialog _____
 Questel/Orbit _____
 Dr.Link _____
 Lexis/Nexis _____
 Sequence Systems abss03
 WWW/Internet _____
 Other (specify) abss04

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 13, 2001, 18:54:41 : Search time 2260.72 Seconds
(without alignments)
4287.580 Million cell updates/sec

Title: US-09-481-990-1
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Scoring table: IDENTITY_NOC
Gapop 10.0 , Gapext 1.0

Searched: 118133 seqs, 2558875100 residues

Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 2
 LOCUS HSU76996 1860 bp mRNA PRI 29-JAN-1998
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 complete cds.
 ACCESSION U76996.1 GI:281119

KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 1860)
 Goldstein,S.A., Wang,K.W., Iian,N. and Pausch,M.H.
TITLE Sequence and function of the two P domain potassium channels:
 implications of an emerging superfamily
 J. Mol. Med. 76 (1), 13-20 (1998)
JOURNAL 98122696
MEDLINE 2 (bases 1 to 1860)
REFERENCE Goldstein,S.A.N.
AUTHORS Submitted (01-NOV-1996) Departments of Pediatrics and Cellular and
 Molecular Physiology, Yale University School of Medicine, Boyer
 Center for Molecular Medicine, 295 Congress Avenue, New Haven, CT
 06536, USA
JOURNAL

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RESULT 3
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ACCESSION U90065
VERSION U90065.1 GI:1916294
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SOURCE human.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1224)
AUTHORS Desir,G.V., Orias,M. and Freeman,T.
TITLE The cloning of a human potassium channel with two pores
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1224)
AUTHORS Desir,G.V., Orias,M. and Freeman,T.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1997) Internal Medicine, Yale University, 333
Cedar St., New Haven, CT 06510, USA

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 QY 1824 GATTTCTTTTATTAAGAAATCAAGAGTCTCAATTAATTAATTAATTAATTAATTA 1883
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 QY 1884 AAAAAAAAAA 1894
 Db 1943 TCAAGAGAAA 1953

RESULT 5
 AL356357/c
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 DEFINITION Homo sapiens chromosome 1 clone RP4-550P15, *** SEQUENCING IN
 ACCESSION AL356357
 VERSION AL356357.12 GI:10715989
 KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 119793)
 AUTHORS Donnelly, S.
 TITLE Direct Submission
 JOURNAL Submitted (04-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 On Oct 6, 2000 this sequence version replaced gi:10045423.
 COMMENT
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 Project Information
 Center project name: dj550P15
 Summary Statistics
 Assembly program: XGAP4; version 4.5
 Sequencing vector: plasmid; L08752; 100% of reads
 Chemistry: Dye-terminator ET-amersham; 29% of reads
 Dye-terminator Big Dye; 70% of reads
 Consensus quality: 119154 bases at least Q40

TITLE
JOURNAL
COMMENT

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tessier, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J.,
Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (16-MAR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On May 28, 2000 this sequence version replaced gi:7651989.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center clone name: 274_P-19

Sequencing vector: M13: M77815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 160532 bases at least Q40

Consensus quality: 16189 bases at least Q30

Consensus quality: 168374 bases at least Q20

Insert size: 171000; agarose-gel

Quality coverage: 4.1 in Q20 bases; agarose-gel

Quality coverage: 4.2 in Q20 bases; sum-of-coverage

* NOTE: This is a 'working draft' sequence. It currently
* consists of 23 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

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* 1272 2617: contig of 1346 bp in length
* 2618 2717: gap of 100 bp
* 2718 4098: contig of 1381 bp in length
* 4099 4198: gap of 100 bp
* 4199 6035: contig of 1837 bp in length
* 6036 6135: gap of 100 bp
* 6136 8540: contig of 2405 bp in length
* 8541 8640: gap of 100 bp
* 8641 11132: contig of 2492 bp in length
* 11133 11232: gap of 100 bp
* 11233 14867: contig of 3635 bp in length
* 14868 14967: gap of 100 bp
* 14968 17745: contig of 2778 bp in length
* 17746 17845: gap of 100 bp
* 17846 18890: contig of 1045 bp in length
* 18891 18990: gap of 100 bp
* 18991 21784: contig of 2794 bp in length
* 21785 21884: gap of 100 bp
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* 25349 25448: gap of 100 bp
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* 31429 31528: gap of 100 bp
* 31529 38131: contig of 6603 bp in length
* 38132 38231: gap of 100 bp
* 38232 44571: contig of 6340 bp in length
* 44572 44671: gap of 100 bp
* 44672 50542: contig of 5871 bp in length
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FEATURES
source

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* 82309 82408: gap of 100 bp
* 82409 92547: contig of 10139 bp in length
* 92548 92647: gap of 100 bp
* 92648 109897: contig of 17250 bp in length
* 109898 109997: gap of 100 bp
* 109998 127653: contig of 17656 bp in length
* 127654 127753: gap of 100 bp
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Db	96232	CACAGGTATACCGTCTACTTGGCTTATTGCCATGTTGGTAGTTC	TGGAACCTCTGTGA	96291
QY	989	ACTCCATAGCTGAAAAAATTCAGAAAAATGTTCTATGTGAAG	AAGACACAGCAGAGA	1048
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QY	1049	TCAGGTGCACATCATAGAGCATGACCACCTGCTTCCTCCCTG	ATCACAGACACAGCAGC	1108
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QY	1109	TGGCATGGAAGAGGACACGAAACAAATGAGCCTTTTGAGCC	ACCCAGTCATCTGCC	1168
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QY	1169	CGTGGATGGCCCTGCAAAACATGAGCGTAGATTGTTGCAT	TATGCTAGACACAGG	1228
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QY	1409	TGTCCACCTTAAATTCATATGTGACAAAAATTTCTCGA	ACCTTAATAGAGAGAGAACTACT	1468
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LOCUS				

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DEFINITION Homo sapiens chromosome 1 clone RP11-528D17, *** SEQUENCING IN
ACCESSION AL360006
VERSION AL360006.5 GI:10178597
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE. 1 (bases 1 to 174629)
AUTHORS Burton,J.
JOURNAL Direct Submission
Submitted (12-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
requests: clonerequests@sanger.ac.uk
On Sep 16, 2000 this sequence version replaced gi:9844026.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BA528D17
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 167120 bases at least Q40
Consensus quality: 170054 bases at least Q30
Consensus quality: 171743 bases at least Q20
Insert size: 173229; sum-of-contigs
Insert size: 185723; 5.5% error; agarose-fp
Quality coverage: 4.45x in Q20 bases; sum-of-contigs Quality
coverage: 4.21x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 1 11804: contig of 11804 bp in length
* 11905 11904: gap of 100 bp
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Location/Qualifiers

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QY	1829	CTCTTTTATACAAAGATCCAGAGTTCCTATCAATTAATTAAGGGGAATATATAA	1882
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VERSION	AF022819				
KEYWORDS	AF022819..1	GI:4103371			
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ORGANISM	Rattus norvegicus				
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AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				
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	Gan,L., Jolmer,W.J., Quinn,A.M., Wang,L.-Y., Hughes,T. and				
	Kaczmarek,L.K.				
TITLE	Cloning and localization of rTWIK, a putative potassium channel				
JOURNAL	with two P domains				
REFERENCE	Unpublished				
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ACCESSION      AX020359
VERSION      AX020359.1 GI:10044093
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 2180)
AUTHORS      Partisetti, M.
TITLES      Two P domains potassium channel
JOURNAL      Patent: WO 936529-A-22-JUL-1999;
SANOFI SYNTHELABO (FR); PARTISETTI MICHEL (FR)
FEATURES
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BASE COUNT      374 a 669 c 645 g 492 t
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Query Match      12.5%; Score 237; DB 51; Length 2180;
Best Local Similarity 56.9%; Pred. No. 7.7e-25;
Matches 463; Conservative 0; Mismatches 335; Indels 15; Gaps 1;
QY      203 CAGCTGTGCTGCGCCGCTGTGAGAGCGGACCGCTCGCTGTGCTTGGCTTCTGTGT 262
Db      46 CAGGGCTCCGGGGGTCCGGGTGGTCATGCGAGAGGGGCGCCTTCTGCGGGCGCTT 105
QY      263 GCTGGGCTACCTTCTCTACCTGTGTCGCGCAGTGTCTTCCCTCGGTGAGAGTCCG 322
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ACCESSION      A94721
VERSION      A94721.1 GI:6778986
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 2180)
AUTHORS      Partisetti, M.
TITLES      TWIK-1 related two domains potassium channel
JOURNAL      Patent: EP 0930364-A-21-JUL-1999;
SYNTHELABO (FR)
FEATURES
Source      Location/Qualifiers
BASE COUNT      374 a 669 c 645 g 492 t
ORIGIN
Query Match      12.5%; Score 237; DB 81; Length 2180;
Best Local Similarity 56.9%; Pred. No. 7.7e-25;
Matches 463; Conservative 0; Mismatches 335; Indels 15; Gaps 1;
QY      203 CAGCTGTGCTGCGCCGCTGTGAGAGCGGACCGCTCGCTGTGCTTCCGCTTCTGTGT 262
Db      46 CAGGGCTCCGGGGGTCCGGGTGGTCATGCGAGAGGGGCGCCTTCTGCGGGCGCCTT 105
QY      263 GCTGGGCTACTTGTCTCTACCTGTGTCGCGCAGTGTCTTCTCTCGGTGAGAGTCCG 322
Db      106 GCGCGGTACGCGCGGACTGTGTGCGCGCGCTGTGTGCGCGGTGAGAGGGGCG 165
QY      323 CTATGAGAGACTCTCTGCGCGAGAGCTGTGCGCAAGCTGAAAGCGACTTCTTGAGAGCA 382
Db      166 GCACGAGAGCGAGGCTCGGAGCCGAGCTGAGAGCCTGTGCGCGCAGCTGTCTGAGCGCAG 225
QY      383 CGAGTGTCTGTGTGAGAGAGCTGTGAGAGCACTTCTGCGCGCGGTGCTGTGAGCGCAGCAA 442
Db      226 CCGGTGTGTGCGCGCGCGCGCGCTGTGAGCGCTTGTGTGAGCGAGTGTGTGCGCGCGAGCG 285

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OY	443	CTACGGCGCTGCGGTGCGTCAGACAGCGCTGGGGCAACTGGAA-----CTG	487
Db	286	GCTGGGGCGGGTCTTGTTCCTTGTCTTAACGCTTGGGGTCCGCCAACCCCTGGACCCCGCTG	345
OY	488	GGACCTTCAACCTCCCGCGCTCTCTTCCTGGCAGACAGCCGTCTCCACACAGATTATGGCA	547
Db	346	GGACTTGCGCCTCTGCTCTCTTCTTCCGCAAGACGCTATACACACCGTGGGGTATGGGTA	405
OY	548	CACCGTGCCCTTGTGCAGATGAGGTAAAGCCCTTGCATCATCTACTCGCTCATTGGCAT	607
Db	406	CACACAGCGCATGTGATGATGAGGGGCAAGCGCTTCCATGCGCTTTGCGCTCCGGGCGT	465
OY	608	TCCCTTACCCCTCGTGTTCCTCGAAGGGGTGGTGGTCACAGCATCACGCTGACGCAACCG	667
Db	466	GCCGACCAACATGCTGCTGCTGACCGGCTAGGCCACAGCGCTG1CACTGCTGCTGACTCA	525
OY	668	CAGCGCCGGTCTCTTACTTCCACATCCGCTGGGGCTTCTCCAAAGCAGTGTGGCCATGCT	727
Db	526	CGTGCCCGCTGTCTTGGGTGAGACATGCGTTGGGGCTGGGACCCCGGGGGCGGCGTCTG	585
OY	728	CCATGCGGTCTCCTTGGGTTGTGCATGTGTCTGCTTCTTCTCATCCCGGCGCTGT	787
Db	586	GCACTTGGTGCGCCTGTGTGGGGGCTGATGACCGCTGCTGCTTCTTGGTGGCGGCTGTAT	645
OY	788	CTTCTCACTCCTGGAGATATACGTGGAACTCCGGAATCCTTTTATTTTGTTTATATTC	847
Db	646	CTTTTCCCATCTTCAGAGAGCGCTGAGACCTTCTTGGAGCCCTTCTACTCTTGTCTTATCTC	705
OY	848	CCTGAGCACAATTGGCCTGGGGGATTAATGTGCGTGGGGAAGGCTACAAATCAAAAATTGAC	907
Db	706	TCTGTCCACCAATGGCGCTGGGCGACTACGTGACCCGGGGAGAGGCCCTTGGCAGCCGCTACCG	765
OY	908	AGAGCTCTATAAGATTGGGATCACTGTTAACGTGCTACTTGGCCCTTAATGCCATGTTGGT	967
Db	766	GGCCCTCTACACAGGTGCTGTGTCACAGCTCACTCTTCCGTGGGCCGTGGTGGCAGATGTGCT	825
OY	968	AGTTCTGGAACCTTCTGTGAACCTCCATCGATGACT	1000
Db	826	GGTGTGAGACCTTCCGCCACGCTCCGCACT	858

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